

**Amendments to the Claims:**

This listing of claims will replace all prior versions and listings of claims in the application:

**Listing of Claims:**

1. (Currently Amended) A method for eliminating indistinguishable differentials from a direct comparison of a pair of ~~samples, data matrices comprising a plurality of data points, wherein each data point in the first matrix of the pair has a corresponding data point in the second matrix of the pair,~~ the method comprising:

- (a) measuring a property of a first sample and a second sample;
- (b) comparing the measured property of the first and second samples to identify differences between the measured property of the first sample and the second sample;
- (c) generating a first data matrix and second data matrix for each sample having a plurality of data points, wherein each data point in the first matrix has a corresponding data point in the second matrix, and wherein each data point has an intensity value corresponding to the measured property of the sample;
- (d) ranking the data points of each matrix from highest to lowest according to intensity value such that a plot of rank versus intensity value of the data points for each matrix provides an experimental curve for each matrix;
- [(b)] (e) fitting a smooth curve to each experimental curve to provide a model curve for each matrix, each model curve comprising a first section separated from a second section by an inflection point;
- [(c)] (f) eliminating any pair of corresponding data points for which each data point of the pair is below the inflection point of its model curve, thereby eliminating indistinguishable differentials from a direct comparison of the pair of samples; and

[(d)] (g) eliminating any pair of corresponding data points for which the rank of each data point of the pair is below a selected cutoff rank between  $r_{\min}$  and  $r_{\max}$ , where  $r_{\min}$  is the rank of the data point at the minimum of the derivative of ~~one each~~ of the model curves and  $r_{\max}$  is the rank of the highest ranking data point on each of the model curves, thereby eliminating indistinguishable differentials from a direct comparison of the pair of samples.

2. (Currently Amended) The method of claim 1, wherein each model curve has an analytical rank determined by the equation:

$$f'(\text{analytical rank}) = C ((f(r_{\max})/r_{\max})),$$

where  $f'(\text{analytical rank})$  is the value of the first derivative of each of the model curves at the analytical rank, C is a constant,  $r_{\max}$  is the rank of a data point having a rank higher than the cutoff rank[[CR]] on each of the model curves, and  $f(r_{\max})$  is the value of each of the model curves at  $r_{\max}$ ;

and further wherein the cutoff rank is the larger analytical rank of the two model curves.

3. (Currently Amended) The method of claim 1, wherein  $r_{\max}$  is the rank of a data point having an intensity in the upper 30% of each of the model curves.

4. (Currently Amended) The method of claim 1, wherein  $r_{\max}$  is the rank of the highest ranking data point on each of the model curves.

5. (Original) The method of claim 1, further comprising normalizing the model curves by transforming the intensity values for the data points in one of the model curves to become equal to the intensity values of the data points of the same rank in the other model curve.

6. (Original) The method of claim 5, wherein the intensity values for the model curve corresponding to the less noisy data matrix are transformed to become equal to the intensity values of model curve corresponding to the noisier data matrix.

7. (Currently Amended) The method of claim 1, wherein the model curves are generated by fitting the experimental curves with the equation:

$$f(x) = \left( \frac{a_1}{x + a_2} + \frac{x}{r_{\max} - x + a_3} - a_4 \right) * a_5 * \left( \frac{1}{1 + \left( \frac{a_7}{x} \right)^{a_6}} + \frac{a_8}{1 + \left( \frac{a_{10}}{x} \right)^{a_9}} - \frac{a_{11}}{x + a_{12}} \right) * \left( 1 + \frac{a_{13}}{1 + \left| 1 - \frac{a_{15}}{x} \right|^{a_{14}}} \right) + \left( \frac{1}{1 + \left( \frac{a_{17}}{x} \right)^{a_{16}}} - a_{18} \right) * a_{19}$$

where  $x$  and  $f(x)$  refer to the rank and logarithmic value of the intensity at rank  $x$ , respectively,  $(a_1, \dots, a_{19})$  are variables **that vary between the model curves** and  $r_{\max}$  is the rank of the highest ranking data point in **the each** data matrix.

8. (Original) The method of claim 2, wherein  $C$  has a value from about 0.3 to about 0.4.

9. (Original) The method of claim 2, wherein  $C$  has a value from about 0.35 to about 0.37.

10. (Currently Amended) The method of claim 1, further comprising measuring a background level ~~for each data points~~ in each matrix and eliminating any pair of corresponding data points for which at least one data point of the pair has a background level that lies outside two or more standard deviations from the mean value of the background measurements for its matrix.

11. (Original) The method of claim 1, wherein each data matrix is generated from an individual sample.

12. (Original) The method of claim 1, wherein each data matrix is generated from a composite sample comprising no more than about 100 individual samples.

13. (Currently Amended) The method of claim 1, wherein the data matrices are generated from biological samples and the data points represent the ~~expression levels~~ amount of biomolecules produced by the biological samples.

14. (Currently Amended) The method of claim 13, wherein the biological samples are selected from the group consisting of cell samples, tissue samples, biological fluid samples, DNA samples and RNA samples.

15. (Currently Amended) The method of claim 1, wherein the data matrices are generated from **samples comprising an extract or derivative of a cell, the measured property is gene expression,** ~~a gene expression profiling experiment~~ and the data points represent gene expression levels.

16. (Currently Amended) The method of claim 1, wherein the data matrices are generated from **samples comprising an extract or derivative of a cell, the measured property is protein expression,** ~~a protein expression profiling experiment~~ and the data points represent protein expression levels.

17. (Currently Amended) The method of claim 1, wherein the data matrices are generated from **samples comprising an extract or derivative of a cell, the measured property is nucleic acid expression,** ~~a nucleic acid sequence expression profiling system~~ and the data points represent ~~oligonucleotide~~ **nucleic acid** expression levels.

18. (Currently Amended) A method for eliminating false differentials from a direct comparison of three or more replicate data matrix pairs, each data matrix comprising a plurality of data points, wherein each data point in the first matrix of the pair has a corresponding data point in the second matrix of the pair and each pair of corresponding data points in each matrix pair has a corresponding pair of corresponding data points in every other matrix pair, the method comprising:

- (a) eliminating indistinguishable differentials from the data matrices according to the method of claim 1;
- (b) determining an intensity ratio for each remaining pair of corresponding data points in each data matrix pair, wherein each ratio is categorized as less than one, greater than one, or equal to one; and
- (c) eliminating any corresponding pairs of corresponding data points for which the intensity ratios for the corresponding pairs fall into the same category for less than one half of the corresponding pairs, **thereby eliminating false differentials from a direct comparison of three or more replicate data matrix pairs.**

19. (Original) The method of claim 18, comprising eliminating corresponding pairs of corresponding data points if the intensity ratios for the corresponding pairs fall into the same category for less than 75 percent of the corresponding pairs.

20. (Original) The method of claim 18, comprising eliminating corresponding pairs of corresponding data points if the intensity ratios for the corresponding pairs fall into the same category for less than 100 percent of the corresponding pairs.

21. (Original) The method of claim 18, further comprising eliminating any data points whose  $\log_2(\text{intensity ratio})$  values lie outside the largest standard deviation of all the remaining  $\log_2(\text{intensity ratio})$  values multiplied by a constant.

22. (Original) The method of claim 21, wherein the constant is at least about 2.

23. (Original) The method of claim 18, wherein the intensity ratios for the remaining data points comprise no more than 1% false differentials.

24. (Original) The method of claim 18, wherein the intensity ratios for the remaining data points comprise no more than 0.1% false differentials.

25. (Original) The method of claim 18, wherein the intensity ratios for the remaining data points comprise no more than 0.01% false differentials.

26. (Currently Amended) The method of claim 18, wherein the data matrices are generated from **samples comprising an extract or derivative of a cell, the measured property is gene expression,** a gene expression profiling experiment and the intensity ratios represent gene expression ratios.

27. (Original) The method of claim 26, wherein the gene expression ratios remaining after the method is applied provide information about gene function behind a biological phenotype.

28. (Original) The method of claim 26, wherein the gene expression ratios remaining after the method is applied provide information about the genetic networks behind a biological phenotype.

29. (Withdrawn) A method for measuring the quality of a direct comparison of a pair of data matrices comprising a plurality of data points, wherein each data point in the first matrix of the pair has a corresponding data point in the second matrix of the pair, the method comprising:

(a) eliminating indistinguishable differentials from the data matrices according to the method of claim 1; and

(b) calculating a noise factor (NF) for the pair of matrices according to the equation:

$$NF = \sqrt{\frac{\sum_{i=1}^n (r_{1i} - r_{2i})^2}{n}} * \frac{K}{(r_{\max} - CR)}$$

wherein CR is the cutoff rank, n is the total number of remaining data points whose ranks are larger than CR in both arrays,  $r_{\max}$  is the rank of a data point having a rank higher than CR,  $r_{1i}$

is the rank of data point  $i$  in the first data matrix of the pair,  $r_{2i}$  is the rank of the corresponding data point in the second data matrix of the pair, and  $K$  is a constant.

30. (Withdrawn) The method of claim 29, wherein  $r_{\max}$  is the rank of a data point having an intensity in the upper 30% of the model curve.

31. (Withdrawn) The method of claim 29, wherein  $r_{\max}$  is the rank of the highest ranking data point on the model curve.

32. (Withdrawn) The method of claim 29, wherein the data matrices are generated from biological samples and the data points represent the expression levels of biomolecules produced by the biological samples.

33. (Withdrawn – Currently Amended) The method of claim 29, wherein the data matrices are generated from **samples comprising an extract or derivative of a cell, the measured property is gene expression,** ~~a gene expression profiling experiment~~ and the intensity ratios represent gene expression ratios.

34. (Withdrawn) The method of claim 33, wherein the gene expression ratios remaining after the method is applied provide information about gene function behind a biological phenotype.

35. (Withdrawn) The method of claim 33, wherein the gene expression ratios remaining after the method is applied provide information about the genetic networks behind a biological phenotype.

36. (New) The method of claim 1, wherein the samples are biological samples.

37. (New) The method of claim 36, wherein the biological sample is a cell, cell line, cell culture, tissue sample, organ, fluid or excretion of a living thing.

38. (New) The method of claim 36, wherein the biological sample is an extract or derivative selected from the group consisting of cDNA, mRNA, DNA, oligonucleotides, or proteins.
39. (New) The method of claim 1, wherein the samples are chemical samples and the measured property is a chromatographic profile.
40. (New) The method of claim 1, wherein the measured property is seismic activity.
41. (New) The method of claim 1, wherein the measured property is economic information.
42. (New) The method of claim 1, wherein the measured property is thermal gravimetric information.
43. (New) The method of claim 1, wherein the measured property is a chemical or biological property of the sample.
44. (New) The method of claim 1, wherein the measured property comprises the structure, composition, or dynamics of the sample.